

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/561, 084
Source: IFWP
Date Processed by STIC: 01/04/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/561, 084

CRF Edit Date: 01/04/06
Edited by: DA

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

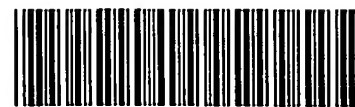
___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

/ Deleted: invalid beginning/end-of-file text ; page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



IFWP

RAW SEQUENCE LISTING

DATE: 01/04/2006

PATENT APPLICATION: US/10/561,084

TIME: 09:40:52

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01042006\J561084.raw

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3 <110> APPLICANT: Peter Christian MORRIS
4     Yvonne STAHL
6 <120> TITLE OF INVENTION: Plant Limit Dextrinase Inhibitor
8 <130> FILE REFERENCE: 13101/49101
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/561,084
C--> 11 <141> CURRENT FILING DATE: 2005-12-16
13 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/002583
W--> 14 <151> PRIOR FILING DATE: 17-JUN-2004
16 <150> PRIOR APPLICATION NUMBER: GB 0313998.7
W--> 17 <151> PRIOR FILING DATE: 17-JUN-2003
19 <160> NUMBER OF SEQ ID NOS: 25
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 517
25 <212> TYPE: DNA
26 <213> ORGANISM: Hordeum vulgare
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (14)..(457)
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34           Met Ala Ser Asp His Arg Arg Phe Val Leu Ser Gly
35           1           5           10
37 gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc gcc gcc acc ctg gag agc      97
38 Ala Val Leu Leu Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser
39           15           20           25
41 gtc aag gac gag tgc caa cca ggg gtg gac ttc ccg cat aac ccg tta      145
42 Val Lys Asp Glu Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu
43           30           35           40
45 gcc acc tgc cac acc tac gtg ata aaa cgg gtc tgc ggc cgc ggt ccc      193
46 Ala Thr Cys His Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro
47 45           50           55           60
49 agc cgg ccc atg ctg gtg aag gag cgg tgc tgc cgg gag ctg gcg gcc      241
50 Ser Arg Pro Met Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala
51           65           70           75
53 gtc ccg gat cac tgc cgg tgc gag gcg ctg cgc atc ctc atg gac ggg      289
54 Val Pro Asp His Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly
55           80           85           90
57 gtg cgc acg ccg gag ggc cgc gtg gtt gag gga cgg ctc ggt gac agg      337
58 Val Arg Thr Pro Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg
59           95          100          105
61 cgt gac tgc ccg agg gag gag cag agg gcg ttc gcc gcc acg ctt gtc      385
62 Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val

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63      110      115      120
65 acg gcg gcg gag tgc aac cta tcg tcc gtc cag gag ccg gga gta cgc 433
66 Thr Ala Ala Glu Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg
67 125      130      135      140
69 ttg gtg cta ctg gca gat gga tga cgatcgaaat gcgccaaggt aatgaagcgg 487
70 Leu Val Leu Leu Ala Asp Gly
71      145
73 agtactgtat acagaataaaa agtactcgag 517
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 147
78 <212> TYPE: PRT
79 <213> ORGANISM: Hordeum vulgare
81 <400> SEQUENCE: 2
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83 1      5      10      15
84 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
85      20      25      30
86 Cys Gln Pro Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
87      35      40      45
88 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
89      50      55      60
90 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Pro Asp His
91 65      70      75      80
92 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
93      85      90      95
94 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
95      100      105      110
96 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
97      115      120      125
98 Cys Asn Leu Ser Ser Val Gln Glu Pro Gly Val Arg Leu Val Leu Leu
99      130      135      140
100 Ala Asp Gly
101 145
105 <210> SEQ ID NO: 3
106 <211> LENGTH: 672
107 <212> TYPE: DNA
108 <213> ORGANISM: Hordeum vulgare
110 <220> FEATURE:
111 <221> NAME/KEY: CDS
112 <222> LOCATION: (39)..(482)
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116      Met Ala Ser Asp His Arg
117      1      5
119 cgc ttc gtc ctc tcc ggc gcc gtc ttg ctc tcg gtc ctc gcc gtc gcc 104
120 Arg Phe Val Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala Val Ala
121      10      15      20
123 gcc gcc acc ttg gag agc gtc aag gac gag tgc caa cta ggg gtg gac 152
124 Ala Ala Thr Leu Glu Ser Val Lys Asp Glu Cys Gln Leu Gly Val Asp

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125          25          30          35
127 ttc ccg cat aac ccg tta gcc acc tgc cac acc tac gtg ata aaa cgg 200
128 Phe Pro His Asn Pro Leu Ala Thr Cys His Thr Tyr Val Ile Lys Arg
129          40          45          50
132 gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg tgc 248
133 Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg Cys
134 55          60          65          70
136 tgc cgg gag ctg gcg gcc gtc ccg gat cac tgc cgg tgc gag gcg ctg 296
137 Cys Arg Glu Leu Ala Ala Val Pro Asp His Cys Arg Cys Glu Ala Leu
138          75          80          85
140 cgc atc ctc atg gac ggg gtg cgc acg ccg gag ggc cgc gtg gtt gag 344
141 Arg Ile Leu Met Asp Gly Val Arg Thr Pro Glu Gly Arg Val Val Glu
142          90          95          100
144 gga cgg ctc ggt gac agg cgt gac tgc ccg agg gag gag cag agg gcg 392
145 Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Glu Gln Arg Ala
146          105          110          115
148 ttc gcc gcc acg ctt gtc acg gcg gcg gag tgc aac cta tcg tcc gtc 440
149 Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Ser Ser Val
150          120          125          130
152 cag gcg ccg gga gta cgc ttg gtg cta ctg gca gat gga tga 482
153 Gln Ala Pro Gly Val Arg Leu Val Leu Leu Ala Asp Gly
154 135          140          145
156 cgatgcaaat gcgccaaggt aatgaagcgg agtactgtat acagaataaaa agtactcgag 542
158 tgaaaacaaa ctcataaata aaccttgtga gatgtatgcg tatgatctat ggtgtggaca 602
160 gttaaattgt ggccgattga tgaataaaaa aggttggaac aaattaaatt gttgtgggtt 662
162 catatactat 672
165 <210> SEQ ID NO: 4
166 <211> LENGTH: 147
167 <212> TYPE: PRT
168 <213> ORGANISM: Hordeum vulgare
170 <400> SEQUENCE: 4
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172 1          5          10          15
173 Ser Val Leu Ala Val Ala Ala Ala Thr Leu Glu Ser Val Lys Asp Glu
174          20          25          30
175 Cys Gln Leu Gly Val Asp Phe Pro His Asn Pro Leu Ala Thr Cys His
176          35          40          45
177 Thr Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met
178          50          55          60
179 Leu Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Ala Val Pro Asp His
180 65          70          75          80
181 Cys Arg Cys Glu Ala Leu Arg Ile Leu Met Asp Gly Val Arg Thr Pro
182          85          90          95
183 Glu Gly Arg Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro
184          100          105          110
185 Arg Glu Glu Gln Arg Ala Phe Ala Ala Thr Leu Val Thr Ala Ala Glu
186          115          120          125
187 Cys Asn Leu Ser Ser Val Gln Ala Pro Gly Val Arg Leu Val Leu Leu
188          130          135          140

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TIME: 09:40:52

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01042006\J561084.raw

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189 Ala Asp Gly
190 145
194 <210> SEQ ID NO: 5
195 <211> LENGTH: 621
196 <212> TYPE: DNA
197 <213> ORGANISM: Triticum aestivum
199 <220> FEATURE:
200 <221> NAME/KEY: CDS
201 <222> LOCATION: (45)..(506)
203 <400> SEQUENCE: 5
204 ggatgaggag gagatgcaac ttgtcaacga caaataaaact atca atg gca tcc aac 56
205                                     Met Ala Ser Asn
206                                     1
208 cat cgt cgc ttc ctc ctc tcc ggc gcc gtc ttg ctc tca gtc ctc gcc 104
209 His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu Ser Val Leu Ala
210   5          10          15          20
212 gcc gtg gcc gcc ctg gag agc gtt gag gac gag tgc cag cca ggg gtg 152
213 Ala Val Ala Ala Leu Glu Ser Val Glu Asp Glu Cys Gln Pro Gly Val
214          25          30          35
216 gcc ttc ccg cac aac gca tta gcc acc tgc cac acc tac gtg atc aaa 200
217 Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr Tyr Val Ile Lys
218          40          45          50
220 cgg gtc tgc ggc cgc ggt ccc agc cgg ccc atg ctg gtg aag gag cgg 248
221 Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu Val Lys Glu Arg
222          55          60          65
224 tgt tgc cgg gag ctg gcg gtc gtc ccg gat tac tgc cgg tgc gag gca 296
225 Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys Arg Cys Glu Ala
226          70          75          80
228 ctg cgc gtc ctc atg gat ggg gtg cgc gcg gag gag ggc cac gtg gtg 344
229 Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu Gly His Val Val
230  85          90          95          100
232 gag ggc cgc ctt ggt gac aga cgt gac tgc ccg agg gag gcg cag cgg 392
233 Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg Glu Ala Gln Arg
234          105          110          115
236 gag ttc gcc gcc acg ctg gtc acg gcg gcg gag tgc aac ctg ccg acc 440
237 Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys Asn Leu Pro Thr
238          120          125          130
240 gtc tcg gga gtc ggg agt aca ctt ggt gcg acc ggc aga tgg atg acg 488
241 Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly Arg Trp Met Thr
242          135          140          145
244 atc gaa ttg ccc aag taa tgaagcgatc aagcgaagta ctctactggc 536
245 Ile Glu Leu Pro Lys
246          150
248 agatggagta ctgcatgtag aataaaagta ctcaagtga aacaaataaa taaagcttgt 596
250 gagctgtatg cgtatgaaaa aaaaa 621
253 <210> SEQ ID NO: 6
254 <211> LENGTH: 153
255 <212> TYPE: PRT
256 <213> ORGANISM: Triticum aestivum

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RAW SEQUENCE LISTING

DATE: 01/04/2006

PATENT APPLICATION: US/10/561,084

TIME: 09:40:52

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01042006\J561084.raw

258 <400> SEQUENCE: 6

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259 Met Ala Ser Asn His Arg Arg Phe Leu Leu Ser Gly Ala Val Leu Leu
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262           20           25           30
263 Gln Pro Gly Val Ala Phe Pro His Asn Ala Leu Ala Thr Cys His Thr
264           35           40           45
265 Tyr Val Ile Lys Arg Val Cys Gly Arg Gly Pro Ser Arg Pro Met Leu
266           50           55           60
267 Val Lys Glu Arg Cys Cys Arg Glu Leu Ala Val Val Pro Asp Tyr Cys
268   65           70           75           80
269 Arg Cys Glu Ala Leu Arg Val Leu Met Asp Gly Val Arg Ala Glu Glu
270           85           90           95
271 Gly His Val Val Glu Gly Arg Leu Gly Asp Arg Arg Asp Cys Pro Arg
272           100          105          110
273 Glu Ala Gln Arg Glu Phe Ala Ala Thr Leu Val Thr Ala Ala Glu Cys
274           115          120          125
275 Asn Leu Pro Thr Val Ser Gly Val Gly Ser Thr Leu Gly Ala Thr Gly
276           130          135          140
277 Arg Trp Met Thr Ile Glu Leu Pro Lys
278 145           150

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282 <210> SEQ ID NO: 7

283 <211> LENGTH: 444

284 <212> TYPE: DNA

286 <213> ORGANISM: Hordeum spontaneum

288 <220> FEATURE:

289 <221> NAME/KEY: CDS

290 <222> LOCATION: (1) .. (444)

292 <400> SEQUENCE: 7

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293 atg gcg ttc aag tac cag ctc ctc ctc tcg gcc gcc gtc atg ctc gcc   48
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295   1           5           10           15
297 att ctc gcc gcc act gtc acc agt ttc ggg gat atg tgt gct cca ggg   96
298 Ile Leu Ala Ala Thr Val Thr Ser Phe Gly Asp Met Cys Ala Pro Gly
299           20           25           30
301 gat gcg ttg cca gcc aac cct ctc aga gcc tgc cgc acc tat gtg gtt   144
302 Asp Ala Leu Pro Ala Asn Pro Leu Arg Ala Cys Arg Thr Tyr Val Val
303           35           40           45
305 agt caa atc tgc cat gta ggc cct aga cta tcc acc tgg gac atg aag   192
307 Ser Gln Ile Cys His Val Gly Pro Arg Leu Ser Thr Trp Asp Met Lys
308           50           55           60
310 agg cgg tgc tgc gac gag ctg tcg gcc atc ccg gcg tac tgc aga tgc   240
311 Arg Arg Cys Cys Asp Glu Leu Ser Ala Ile Pro Ala Tyr Cys Arg Cys
312   65           70           75           80
314 gag gcg ctg cgt atc atc atg gat ggg aca gta act tgg cag ggt gtg   288
315 Glu Ala Leu Arg Ile Ile Met Asp Gly Thr Val Thr Trp Gln Gly Val
316           85           90           95
318 ttc ggt gcc tac ttc aag gac atg ccc aac tgc cct agg gtg atg caa   336
319 Phe Gly Ala Tyr Phe Lys Asp Met Pro Asn Cys Pro Arg Val Met Gln

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VERIFICATION SUMMARY

DATE: 01/04/2006

PATENT APPLICATION: US/10/561,084

TIME: 09:40:53

Input Set : A:\pto.da.txt

Output Set: N:\CRF4\01042006\J561084.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD

**Raw Sequence Listing before editing,
for reference only**



IFWP

RAW SEQUENCE LISTING

DATE: 12/30/2005

PATENT APPLICATION: US/10/561,084

TIME: 09:23:53

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12302005\J561084.raw

3 <110> APPLICANT: Peter Christian MORRIS
 4 Yvonne STAHL
 6 <120> TITLE OF INVENTION: Plant Limit Dextrinase Inhibitor
 8 <130> FILE REFERENCE: 13101/49101
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/561,084
 C--> 11 <141> CURRENT FILING DATE: 2005-12-16
 13 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/002583
 W--> 14 <151> PRIOR FILING DATE: 17-JUN-2004
 16 <150> PRIOR APPLICATION NUMBER: GB 0313998.7
 W--> 17 <151> PRIOR FILING DATE: 17-JUN-2003
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed
 (pg-1)

ERRORED SEQUENCES

789 <210> SEQ ID NO: 25
 790 <211> LENGTH: 20
 791 <212> TYPE: DNA
 792 <213> ORGANISM: Artificial Sequence
 794 <220> FEATURE:
 795 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
 797 <400> SEQUENCE: 25
 798 ccatgcctag ggacacactt 20
 E--> 811 (1)

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VERIFICATION SUMMARY

DATE: 12/30/2005

PATENT APPLICATION: US/10/561,084

TIME: 09:23:54

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\12302005\J561084.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:17 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:811 M:254 E: No. of Bases conflict, this line has no nucleotides.